

FASTA searches a protein or DNA sequence data bank
version 3.3t05 March 30, 2000

Please cite:

W.R. Pearson & D.J. Lipman PNAS (1988) 85:2444-2448

```
/tmp.fastaCAAQPaiHi: 995 aa
 >SEQ ID NO:2
 vs  /tmp.fastaDAARPaiHi library
searching /tmp.fastaDAARPaiHi library
```

1008 residues in 1 sequences

FASTA (3.34 January 2000) function [optimized, BL50 matrix (15:-5)] ktup: 20
join: 39, opt: 27, gap-pen: -12/-2, width: 16

Scan time: 0.050

Scan time: 0:050
The best scores are: opt
NM 000096 ACCESSION:NM 000096 NID: gi 4557484 ref (1008) 2671

```
>>NM_000096 ACCESSION:NM_000096 NID: gi 4557484 ref NM_0 (1008 aa)
  initn: 1414 init1: 972 opt: 2671
Smith-Waterman score: 3980; 57.002% identity in 1014 aa overlap (1-992:1-1008)
```

	120	130	140	150	160	170
SEQ	SYHPHGLTYSKENEAHGAIYPDNTTGLQKEVEYLEPGKQTYKWyVEEHQGPGPNDSNCV					

NM_000	TFHSHGITYYKEHE--GAIYPDNTTDFQRADDKVYPGEQTYMLLATEEQSPGEGDGNCV					

	180	190	200	210	220	230	
SEQ	TRIYHSHIDTARDVASGLIGPLILTCKRGTLNGDTEKDIDRSSFLMFSTTDERSWYSDEN	
NM_000	TRIYHSHIDAPKDIASGLIGPLIICKKDSLDEKEKHIDREFVVMFSVVDENFSWYLEDN	180	190	200	210	220	230

	240	250	260	270	280	290
SEQ	IRAF-TESGKINTSDPRFEESMSMQSINGYIYGNLPNLTMCAEDRQWYFVGMGGVADIH					
 :	.. : : ..
NM_000	IKTYCSEPEKVDKDNEFQESNRMYSVNGYTFGSLPGLSMCAEDRVKWYLFGMGNEDVH					
	240	250	260	270	280	290

	300	310	320	330	340	350
SEQ	PVYLRGQTLISRNRHKDTIMLFPSSLEDAFMVAKAPGVWMLGCQ---IHESMQAFFKVS:..: ..:..: ::: ::::: : ::::: . :: ::::::::..					
NM_000	AAFFHGQALTNKNYRIDTINLFATLFDAYMVAQNPGEWMLSCQNLNHLKAGLQAFFFQVQ 300 310 320 330 340 350					

	360	370	380	390	400	410
SEQ	NCQKPSTEAFVTGTHVIHYYIAAKEILWNYAPSGIDFFTKKNLTAAGSKSQLFFERSPTR ...: . . :					
NM_000	ECNKSSSKDNIRGKHVRHYYIAAEEIIWNYAPSGIDIFTKENLTAPGSDSAVFSEQGTR 360 370 380 390 400 410					
	420	430	440	450	460	
SEQ	IGGYKKLIYREYTDASFQTQKAR---EEHLGILGPVFKAEVGQTIKITFYNNASLPLSI :					
NM_000	IGGSYKKLVYREYTDASFTRKERGPEEEHLGILGPVIWAEVGDTIRVTFHNGAYPLSI 420 430 440 450 460 470					
	470	480	490	500	510	520
SEQ	QPPGLHYNKSNEGLFYE---TPGG-STPPPSSHVSPGTTFVYTWEVPKDVGPTSTDPNCL .. : . : : : : : : . : . : . :					
NM_000	EPIGVRFNKNNEGTYYSPNYPQSRSPVPPSASHVAPTTFTYEWTVPKEVGPTNADPVCL 480 490 500 510 520 530					
	530	540	550	560	570	580
SEQ	TWFYYSSVNGKKDINSGLGPPLLICRNGSLGDDGKQKGVDKEFYLLATIFDENESNLLDE . . : . : . :					
NM_000	AKMYYSAVDPTKDIIFTGLIGPMKICKKGSLLHANGRQKDVFKEFYLFPTVFDENESLLLED 540 550 560 570 580 590					
	590	600	610	620	630	640
SEQ	N-RTFITEPENIDKEDTDCQASNKMYISINGYMYGNLPGLDTCLDGNVLWHVFSVGSVEDL . : : : : . :					
NM_000	NIRMFTTAPDQVDKEDEDQFQESNKMHSMNGFMYGNQPLTMCKGDSVVWYLFSAAGNEADV 600 610 620 630 640 650					
	650	660	670	680	690	700
SEQ	HGIYFSGNTFTSLGARRDTIPMFPTYSQTLMPDSIGTFDLVCMTIKHNLGGMKHYHV . : : : : . :					
NM_000	HGIYFSGNTYLWRGERRDATANLFQTSLTLHMWPDTETGTFNVECLTDHYTGGMKQKYTV 660 670 680 690 700 710					
	710	720	730	740	750	760
SEQ	RQCGKPNPDQTQYQEEKIIITIAAEEMEDYSPSRKWENELHHLRRENQTSMYVDRSGTL . : . : . :					
NM_000	NQCRRQSEDSTFYLGERTYY-IAAVEVEWDYSPQREWEKELHHLQEQNVSNAFLDKGEFY 720 730 740 750 760 770					
	770	780	790	800	810	820
SEQ	LGSKYKKVLYRQYDDNTFTNQTKRNEGEKHLDILGPLILLNPGQIIQIIFKNKAARPYSI . :					
NM_000	IGSKYKKVVYRQYTDSTFRVPVERKAEEEHLGILGPQLHADVGDKVKIIFKNMATRPSI 780 790 800 810 820 830					
	830	840	850	860	870	880
SEQ	HAHGVKTNNSTVVPTQPGEIQIYTQWQIPDRTGPTSLDFECIPWFYYSTVSVAKDLHSGLV . :					
NM_000	HAHGVQTESSTVTPTLPGETLTYVWKIPERSGAGTEDSACIPWAWYSTVDQVKDLYSGLI 840 850 860 870 880 890					

	890	900	910	920	930	
SEQ	GPLSVCR	---KDINPN	-IVHRLHFMIFDENESWYFEDSINTYASKPNKVDKENDNFQL			
	::: :::	: :::	. . : . : . : . : . : . : . : . :			
NM_000	GPLIVCRRPYLKVNPRRKLEFALLFLVFDENESWYLDNNIKTYSDHPEKVNKDDEEFIE					
	900	910	920	930	940	950
	940	950	960	970	980	990
SEQ	SNQMHAINGRLFGNNQGITFHVGDVVNWY	LIGIGNEADLHTVHFHGH	SFEYKH	KYLI		
	: :					
NM_000	SNKMHAINGRMFGNLQGLTMHVGDEVNWYLMGMGNEIDLHTVHFHGH	SFQYK	HR			
	960	970	980	990	1000	

995 residues in 1 query sequences

1008 residues in 1 library sequences

Scomplib [version 3.3t05 March 30, 2000]

start: Wed Sep 18 11:16:31 2002 done: Wed Sep 18 11:16:32 2002

Scan time: 0.050 Display time: 1.417

Function used was FASTA